

004220" 666ET363

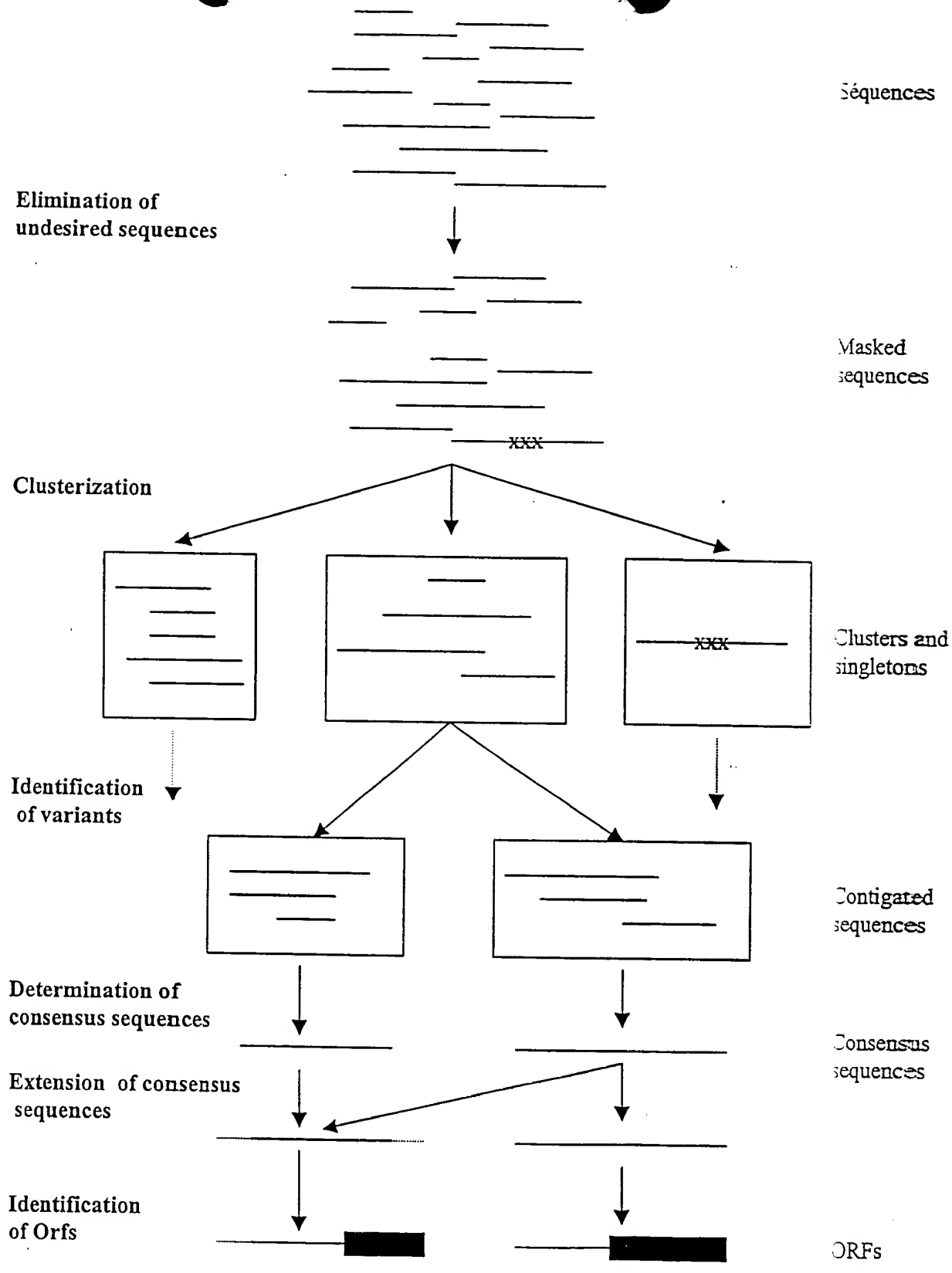


FIGURE 1

004220" 666ET560

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3,5	0,121	0,036	0,467	0,664
4	0,096	0,06	0,519	0,708
4,5	0,078	0,079	0,565	0,745
5	0,062	0,098	0,615	0,782
5,5	0,05	0,127	0,659	0,813
6	0,04	0,163	0,694	0,836
6,5	0,033	0,202	0,725	0,855
7	0,025	0,248	0,763	0,878
7,5	0,021	0,304	0,78	0,889
8	0,015	0,368	0,816	0,909
8,5	0,012	0,418	0,836	0,92
9	0,009	0,512	0,856	0,93
9,5	0,007	0,581	0,863	0,934
10	0,006	0,679	0,835	0,919

FIGURE 2

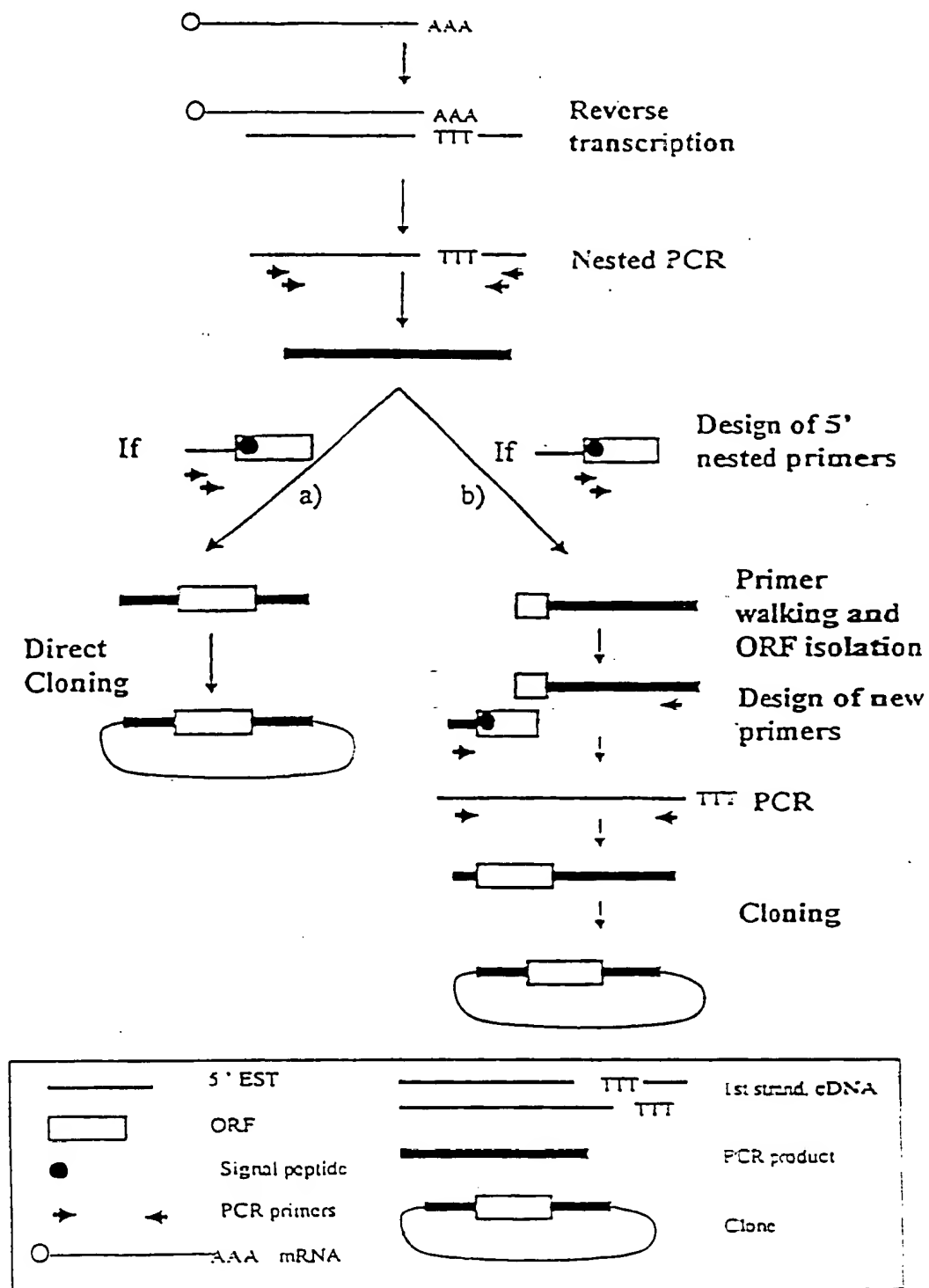


FIGURE 3

Description of promoters structure isolated from SignalTag 5' ESTs

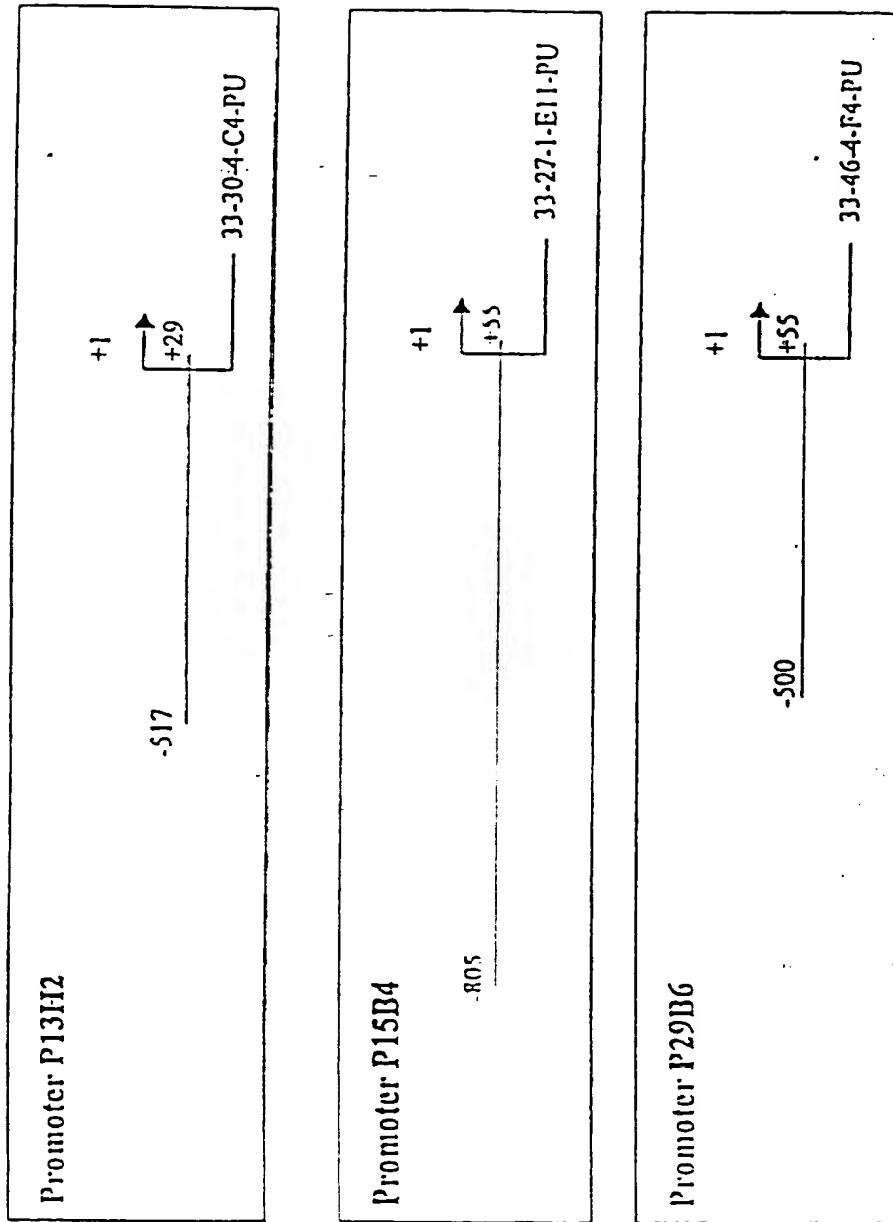


FIGURE 4

Description of Transcription Factor Binding Sites present in promoters isolated from SignalTag sequences

Promoter sequence P13H2 (546 bp):

Matrix	Position	Orientation	Score	Length	Sequence	Location in: SEQ ID NO: 17
CMYB_01	-502	+	0.983	9	TGTCAGTTG	17-25
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC	complement of 18-27
S8_01	-444	-	0.960	11	AATAGAATTAG	complement of 75-85
S8_01	-425	+	0.966	11	AACTAAATTAG	94-104
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG	complement of 129-139
GATA_C	-364	-	0.964	11	AGATAAATCCA	complement of 155-165
CMYB_01	-349	+	0.958	9	CTTCAGTTG	170-178
GATAI_02	-343	+	0.959	14	TTGTAGATAGGACA	176-189
GATA_C	-339	+	0.953	11	AGATAGGACAT	180-190
TAL1ALPHA47_01	-235	+	0.973	16	CATAACAGATGGTAAG	284-299
TALIBETA47_01	-235	+	0.983	16	CATAACAGATGGTAAG	284-299
TALIBETAITF2_01	-235	+	0.978	16	CATAACAGATGGTAAG	284-299
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT	complement of 287-296
GATAI_04	-217	-	0.953	13	TCAAGATAAAGTA	complement of 302-314
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC	393-405
IK2_01	-126	+	0.985	12	AGTTGGGAATTC	393-404
CREL_01	-123	+	0.962	10	TGGGAATTCC	396-405
GATAI_02	-96	+	0.950	14	TCAGTGATATGGCA	423-436
SRY_02	-41	-	0.951	12	TAAACAAAACA	complement of 478-489
E2F_02	-33	+	0.957	8	TTAGCGC	486-493
MZF1_01	-5	-	0.975	8	TGAGGGGA	complement of 514-521

Promoter sequence P15B4 (861 bp):

Matrix	Position	Orientation	Score	Length	Sequence	Location in: SEQ ID NO: 20
NFY_Q6	-748	-	0.956	11	GGACCAATCAT	complement of 60-70
MZF1_01	-738	+	0.962	8	CCTGGGGA	70-77
CMYB_01	-684	+	0.994	9	TGACCGTTG	124-132
VMYB_02	-682	-	0.985	9	TCCAACGGT	complement of 126-134
STAT_01	-673	+	0.968	9	TTCTGGAA	135-143
STAT_01	-673	-	0.951	9	TTCCAGGAA	complement of 135-143
MZF1_01	-556	-	0.956	8	TTGGGGGA	complement of 252-259
IK2_01	-451	+	0.965	12	GAATGGGATTTC	357-368
MZF1_01	-424	+	0.986	8	AGAGGGGA	384-391
SRY_02	-398	-	0.955	12	GAAAACAAAACA	complement of 410-421
MZF1_01	-216	+	0.960	8	GAAGGGGA	592-599
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC	618-627
DELTAEF1_01	-176	+	0.958	11	TCCACCTTCC	632-642
S8_01	5	-	0.992	11	GAGGCAATTAT	complement of 813-823
MZF1_01	16	-	0.986	8	AGAGGGGA	complement of 824-831

Promoter sequence P29B6 (555 bp):

Matrix	Position	Orientation	Score	Length	Sequence	Location in: SEQ ID NO: 23
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT	191-206
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG	193-204
USF_01	-309	+	0.985	12	ACTCACGTGCTG	193-204
USF_01	-309	-	0.985	12	CAGCACGTGAGT	complement of 193-204
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT	complement of 193-204
MYCMA_X_02	-309	-	0.972	12	CAGCACGTGAGT	complement of 193-204
USF_C	-307	+	0.997	8	TCACGTGC	195-202
USF_C	-307	-	0.991	8	GCACGTGA	complement of 195-202
MZF1_01	-292	-	0.968	8	CATGGGGA	complement of 210-217
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT	397-410
CETSIP54_01	-102	+	0.974	10	TCCGGAAGCC	400-409
API_Q4	-42	-	0.963	11	AGTGACTGAAC	complement of 460-470
APIFJ_Q2	-42	-	0.961	11	AGTGACTGAAC	complement of 460-470
PADS_C	45	+	1.000	9	TGTGGTCTC	547-555

FIGURE 5